# PREFACE

This book is a completely revised edition of *Human Evolutionary Genetics*, first published in 2004. We decided to write the first edition because there were no textbooks available covering the areas that interested us. Once we had embarked upon the Herculean task of producing it, we realized why nobody had attempted to summarize this forbiddingly broad and contentious field before. But luckily the reception was positive, one eager person (our ideal reader and not, we point out, one of the authors in disguise) writing on Amazon that "I bought a copy for myself, and another one for my advisor. I have read it twice in a week!" A revised version seemed like a pretty good idea.

We cheerfully imagined that the second edition would be easier to write than the first. How wrong we were. First, all three original authors (MJ, MH, and CTS) had accumulated additional responsibilities that reduced the available time for writing. Second, the field obstinately continued to grow, and scarcely a week went by without some interesting and important development—the genomes of new species, genomewide surveys of human variation, next-generation sequencing and its data tsunami, spectacular ancient DNA discoveries, large-scale population studies, novel statistical methods, archaeological and paleontological revelations—the list goes on. We sometimes wished everyone would just stop working for a bit, so we could catch up. So, our deadline for the second edition passed, was revised, and passed again. HEG1 was becoming more and more out of date. We needed help.

The cavalry duly arrived in the form of two sterling new recruits to the authorial team—EH and TK. They brought their own areas of interest and expertise, but also a more efficient and energetic approach to the writing process, which revitalized the whole project. So, after a lengthy and difficult gestation, here is HEG2.

Following an initial introductory chapter, the book is divided into five sections, allowing it to be read by interested students and researchers from a broad range of backgrounds. "How do we study genome diversity?" (Chapters 2–4) and "How do we interpret genetic variation?" (Chapters 5–6) together provide the necessary tools to understand the rest of the book. The first of these sections surveys the structure of the genome, different sources of genomic variation, and the methods for assaying diversity experimentally. The second introduces the evolutionary concepts and analytical tools that are used to interpret this diversity. The subsequent two sections take an approximately chronological course through the aspects of our current state of knowledge about human origins that we consider most important. The section "Where and when did humans originate?" (Chapters 7–9) first considers our links to our closest living nonhuman relatives, the other great apes, then investigates the genetic changes that have made us

human, and finally details the more recent African origin of our own species. "How did humans colonize the world?" (Chapters 10–14) describes how human genetic diversity is currently distributed globally and then discusses the evidence for early human movements out of Africa, and the subsequent processes of expansion, migration, and mixing that have shaped patterns of diversity in our genomes. Finally, "How is an evolutionary perspective useful?" (Chapters 15–18) demonstrates the wider applications of an evolutionary approach for our understanding of phenotypic variation, the genetics of diseases both simple and complex, and the identification of individuals. Extensive cross-referencing between these sections facilitates different routes through the book for readers with divergent interests and varying amounts of background knowledge.

An important feature is the use of "Opinion Boxes"—short contributions by guest authors who are experts in different aspects of this diverse subject area. These help to give a flavor of scientific enquiry as an ongoing process, rather than a linear accumulation of facts, and encourage the reader to regard the published literature with a more critical eye. Opinions about how data should be interpreted change, and often an objective way to choose between different interpretations is not obvious. This is particularly true of genetic data on human diversity. Many of the debates represented in the Opinion Boxes scattered through this book derive from methodological differences.

Additional resources have been incorporated to permit interested readers to explore topics in greater depth. Each chapter is followed by a detailed bibliography, within which the sources that should be turned to first for more detail are highlighted in purple text. Electronic references to internet sites are given throughout the book, both for additional information and for useful software and databases. We explain specialist terms where they are first used, and include an extensive glossary at the back of the book that defines all terms in the text that are in bold type. At the end of each chapter is a list of questions (some short-answer, and some prose) that allow the reader to test their knowledge as they proceed. Teachers may be interested to know that most of the figures are freely available from the Garland Science Website (www.garlandscience.com) for use in teaching materials.

An obvious difference from the first edition is the presence of two extra chapters, reflecting developments in understanding the human genome in the context of other hominid genomes, and in complex disease. A very welcome development is the availability of full-color printing, which makes complex figures much easier to understand.